



## SEQUENCE LISTING

<110> Godfrey, Wayne  
Buck, David  
Engleman, Edgar G.

<120> Monoclonal Antibodies to a Receptor (ACT-4) on the Surface of Activated CD4+ T-Cells (As Amended)

<130> 16524.010

<140> US 09/852,845  
<141> 2001-05-11

<150> US 08/472,940  
<151> 1995-06-06

<150> US 08/147,784  
<151> 1993-11-03

<160> 2

<210> 1  
<211> 1057  
<212> DNA  
<213> Homo sapiens

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<221> CDS  
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<220>  
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Met Cys Val Gly Ala Arg Arg Leu Gly Arg Gly Pro  
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tgt gcg gct ctg ctc ctc ctg ggc ctg ggg ctg agc acc gtg acg ggg 98  
Cys Ala Ala Leu Leu Leu Gly Leu Gly Leu Ser Thr Val Thr Gly  
15 20 25

ctc cac tgt gtc ggg gac acc tac ccc agc aac gac gac cgg tgc tgc cac 146  
Leu His Cys Val Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His  
30 35 40

gag tgc agg cca ggc aac ggg atg gtg agc cgc tgc agc cgc tcc cag 194  
Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln  
45 50 55 60

aac acg gtg tgc cgt ccg tgc ggg ccg ggc ttc tac aac gac gtg gtc		242	
Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val			
65	70	75	
agc tcc aag ccg tgc aag ccc tgc acg tgg tgt aac ctc aga agt ggg		290	
Ser Ser Lys Pro Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly			
80	85	90	
agt gag ccg aag cag ctg tgc acg gcc aca cag gac aca gtc tgc cgc		338	
Ser Glu Arg Lys Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg			
95	100	105	
tgc cgg ggc acc cag ccc ctg gac agc tac aag cct gga gtt gac		386	
Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp			
110	115	120	
tgt gcc ccc tgc cct cca ggg cac ttc ttc cca ggc gac aac cag gcc		434	
Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala			
125	130	135	140
tgc aag ccc tgg acc aac tgc acc ttg gct ggg aag cac acc ctg cag		482	
Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln			
145	150	155	
ccg gcc agc aat agc tcg gac gca atc tgt gag gac agg gac ccc cca		530	
Pro Ala Ser Asn Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro			
160	165	170	
gcc acg cag ccc cag gag acc cag ggc ccc ccg gcc agg ccc atc act		578	
Ala Thr Gln Pro Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr			
175	180	185	
gtc cag ccc act gaa gcc tgg ccc aga acc tca cag gga ccc tcc acc		626	
Val Gln Pro Thr Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr			
190	195	200	
cg <sup>g</sup> ccc gtg gag gtc ccc ggg ggc cgt gc <sup>g</sup> gtt gcc gcc atc ctg ggc		674	
Arg Pro Val Glu Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly			
205	210	215	220
ctg ggc ctg gtg ctg ggg ctg ctg ggc ccc ctg gcc atc ctg ctg gcc		722	
Leu Gly Leu Val Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala			
225	230	235	
ctg tac ctg ctc cgg agg gac cag agg ctg ccc ccc gat gcc cac aag		770	
Leu Tyr Leu Leu Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys			
240	245	250	
ccc cct ggg gga ggc agt ttc cgg acc ccc atc caa gag gag cag gcc		818	
Pro Pro Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala			
255	260	265	

gac gcc cac tcc acc ctg gcc aag atc tgacctggc ccaccaagg 865  
Asp Ala His Ser Thr Leu Ala Lys Ile  
270 275

ggacgctggg ccccgccagg ctggagcccg gagggctgc tggcgagca gggcaggtgc 925  
aggccgcctg ccccgccacg ctccctggcc aactctgcac cgttctaggt gccgatggct 985  
gcctccggct ctctgcttac gtatgccatg catacctcct gccccgcggg accacaataa 1045  
aaaccttggc ag 1057

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<220>  
<223> deduced amino acid sequence of ACT-4-h-1

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Leu Leu Leu Gly Leu Gly Leu Ser Thr Val Thr Gly Leu His Cys Val  
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Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His Glu Cys Arg Pro  
35 40 45

Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln Asn Thr Val Cys  
50 55 60

Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val Ser Ser Lys Pro  
65 70 75 80

Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly Ser Glu Arg Lys  
85 90 95

Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg Cys Arg Ala Gly  
100 105 110

Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp Cys Ala Pro Cys  
115 120 125

Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala Cys Lys Pro Trp  
130 135 140

Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln Pro Ala Ser Asn

145                    150                    155                    160  
Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro Ala Thr Gln Pro  
165                    170                    175  
Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr Val Gln Pro Thr  
180                    185                    190  
Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr Arg Pro Val Glu  
195                    200                    205  
Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly Leu Gly Leu Val  
210                    215                    220  
Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala Leu Tyr Leu Leu  
225                    230                    235                    240  
Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly  
245                    250                    255  
Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser  
260                    265                    270  
Thr Leu Ala Lys Ile  
275